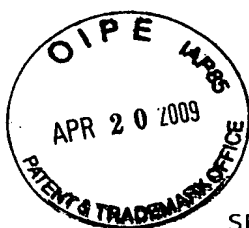Please replace the Sequence Listing now on file with the new Sequence Listing.

SEQUENCE LISTING

<110>   SAHIN, ERINC
        TARALP, ALPAY
        SAYERS, SEHRA

<120>   CIRCULAR RECOMBINANT PLASMID DNA CONSTRUCTS AND THEIR PROTEIN
        PRODUCTS, METHODS OF PREPARATION AND IMMOBILISATION OF PROTEINS
        ON SUPPORT

<130>   U015936-2

<140>   10/550226
<141>   2005-09-20

<150>   PCT/TR2003/000019
<151>   2003-03-20

<160>   12

<170>   PatentIn version 3.3

<210>   1
<211>   733
<212>   DNA
<213>   Aequorea victoria

<220>
<221>   gene
<222>   (17)..(733)
<223>   GFP gene

<400>   1
ggtaccggta gaaaaaatga gtaaaggaga agaacttttc actggagttg tcccaattct   60

tgttgaatta gatggtgatg ttaatgggca caaattttct gtcagtggag agggtgaagg   120

tgatgcaaca tacggaaaac ttacccttaa atttatttgc actactggaa aactacctgt   180

tccatggcca acacttgtca ctactttctc ttatggtgtt caatgctttt cccgttatcc   240

ggatcatatg aaacggcatg acttttttcaa gagtgccatg cccgaaggtt atgtacagga   300

acgcactata tctttcaaag atgacgggaa ctacaagacg cgtgctgaag tcaagtttga   360

aggtgatacc cttgttaatc gtatcgagtt aaaaggtatt gattttaaag aagatggaaa   420

cattctcgga cacaaactcg agtacaacta taactcacac aatgtataca tcacggcaga   480

caaacaaaag aatggaatca aagctaactt caaaattcgc cacaacattg aagatggatc   540

cgttcaacta gcagaccatt atcaacaaaa tactccaatt ggcgatggcc ctgtcctttt   600

accagacaac cattacctgt cgacacaatc tgccctttcg aaagatccca acgaaaagcg   660

tgaccacatg gtccttcttg agtttgtaac tgctgctggg attacacatg gcatggatga   720

gctctacaaa taa   733

<210>   2
<211>   6029

<212> DNA
<213> Artificial sequence

<220>
<223> Empty PETM-11 plasmid

<220>
<221> misc_feature
<222> (1)..(6029)
<223> Empty PETM-11 plasmid

<400> 2

```
atccggatat agttcctcct ttcagcaaaa aacccctcaa gacccgttta gaggccccaa      60

ggggttatgc tagttattgc tcagcggtgg cagcagccaa ctcagcttcc tttcgggctt     120

tgttagcagc cggatctcag tggtggtggt ggtggtgctc gagtgcggcc gcaagcttgt     180

cgacggagct cgaattcgga tccggtacca ctagttagag accaagacac gccttgtgac     240

tgtcctgcag ctttattctc ttgatgctgg tgctggaata gccctcatca ctgccgaggc     300

tctgcatgct gccccgctcg tcagagtcgc tcacactgct gctgctccag tccagatcac     360

ctgtgagata gtccgtgctc tccacgtcaa cgtcgatttc ttccctgtcg gagtcggagc     420

gctccgagga gacggtggag ccgatgctgt ccatccggat cctctcaatg cccagcttct     480

ccagctgcct cttcaggtgt cgctgctctc gctgaagctg gtcgatttgg tgaacggctt     540

ttctgtcaca atcttcaagt ttctttatgt gcaatttggc ttttgttaat aaactcaacg     600

tagtgtgtcg acttgattcg ggtcccagtg gcaccagccc cttcaacttc tccaggcaca     660

agcgaagatg agcccgtcta ttcttctcca tttcattgtg agttgatctg ctactgctgt     720

tattcttttt ggatttgttc ctccgtttta aggcatctct gtccttgttt ttgtatggta     780

acatggaggc ataaccatgt tcagcttctc tctcccgccg ctccagatag tcggccgcct     840

ccagcagcat ctggatgttc atccgaaccg ccgccgccat ggcgccctga aaataaagat     900

tctcagtagt ggggatgtcg taatcgctca tggggtgatg gtgatggtga tgtttcatgg     960

tatatctcct tcttaaagtt aaatcaaaat tatttctaga ggggaattgt tatccgctca    1020

caattcccct atagtgagtc gtattaattt cgcgggatcg agatctcgat cctctacgcc    1080

ggacgcatcg tggccggcat caccggcgcc acaggtgcgg ttgctggcgc ctatatcgcc    1140

gacatcaccg atggggaaga tcgggctcgc cacttcgggc tcatgagcgc ttgtttcggc    1200

gtgggtatgg tggcaggccc cgtggccggg ggactgttgg cgccatctc cttgcatgca     1260

ccattccttg cggcggcggt gctcaacggc ctcaacctac tactgggctg cttcctaatg    1320

caggagtcgc ataagggaga gcgtcgagat cccggacacc atcgaatggc gcaaaacctt    1380

tcgcggtatg gcatgatagc gcccggaaga gagtcaattc agggtggtga atgtgaaacc    1440

agtaacgtta tacgatgtcg cagagtatgc cggtgtctct tatcagaccg tttcccgcgt    1500
```

```
ggtgaaccag gccagccacg tttctgcgaa aacgcgggaa aaagtggaag cggcgatggc    1560

ggagctgaat tacattccca accgcgtggc acaacaactg gcgggcaaac agtcgttgct    1620

gattggcgtt gccacctcca gtctggccct gcacgcgccg tcgcaaattg tcgcggcgat    1680

taaatctcgc gccgatcaac tgggtgccag cgtggtggtg tcgatggtag aacgaagcgg    1740

cgtcgaagcc tgtaaagcgg cggtgcacaa tcttctcgcg caacgcgtca gtgggctgat    1800

cattaactat ccgctggatg accaggatgc cattgctgtg gaagctgcct gcactaatgt    1860

tccggcgtta tttcttgatg tctctgacca gacacccatc aacagtatta ttttctccca    1920

tgaagacggt acgcgactgg gcgtggagca tctggtcgca ttgggtcacc agcaaatcgc    1980

gctgttagcg ggcccattaa gttctgtctc ggcgcgtctg cgtctggctg ctggcataa    2040

atatctcact cgcaatcaaa ttcagccgat agcggaacgg gaaggcgact ggagtgccat    2100

gtccggtttt caacaaacca tgcaaatgct gaatgagggc atcgttccca ctgcgatgct    2160

ggttgccaac gatcagatgg cgctgggcgc aatgcgcgcc attaccgagt ccgggctgcg    2220

cgttggtgcg gatatctcgg tagtgggata cgacgatacc gaagacagct catgttatat    2280

cccgccgtta accaccatca aacaggattt tcgcctgctg gggcaaacca gcgtggaccg    2340

cttgctgcaa ctctctcagg gccaggcggt gaagggcaat cagctgttgc ccgtctcact    2400

ggtgaaaaga aaaaccaccc tggcgcccaa tacgcaaacc gcctctcccc gcgcgttggc    2460

cgattcatta atgcagctgg cacgacaggt ttcccgactg gaaagcgggc agtgagcgca    2520

acgcaattaa tgtaagttag ctcactcatt aggcaccggg atctcgaccg atgcccttga    2580

gagccttcaa cccagtcagc tccttccggt gggcgcgggg catgactatc gtcgccgcac    2640

ttatgactgt cttctttatc atgcaactcg taggacaggt gccggcagcg ctctgggtca    2700

ttttcggcga ggaccgcttt cgctggagcg cgacgatgat cggcctgtcg cttgcggtat    2760

tcggaatctt gcacgccctc gctcaagcct tcgtcactgg tcccgccacc aaacgtttcg    2820

gcgagaagca ggccattatc gccggcatgg cggccccacg ggtgcgcatg atcgtgctcc    2880

tgtcgttgag gacccggcta ggctggcggg gttgccttac tggttagcag aatgaatcac    2940

cgatacgcga gcgaacgtga agcgactgct gctgcaaaac gtctgcgacc tgagcaacaa    3000

catgaatggt cttcggtttc cgtgtttcgt aaagtctgga aacgcggaag tcagcgccct    3060

gcaccattat gttccggatc tgcatcgcag gatgctgctg ctaccctgt ggaacaccta    3120

catctgtatt aacgaagcgc tggcattgac cctgagtgat ttttctctgg tcccgccgca    3180

tccataccgc cagttgttta ccctcacaac gttccagtaa ccgggcatgt tcatcatcag    3240

taacccgtat cgtgagcatc ctctctcgtt tcatcggtat cattaccccc atgaacagaa    3300

atccccctta cacggaggca tcagtgacca aacaggaaaa aaccgccctt aacatggccc    3360

gctttatcag aagccagaca ttaacgcttc tggagaaact caacgagctg gacgcggatg    3420
```

```
aacaggcaga catctgtgaa tcgcttcacg accacgctga tgagctttac cgcagctgcc   3480

tcgcgcgttt cggtgatgac ggtgaaaacc tctgacacat gcagctcccg gagacggtca   3540

cagcttgtct gtaagcggat gccgggagca gacaagcccg tcagggcgcg tcagcgggtg   3600

ttggcgggtg tcggggcgca gccatgaccc agtcacgtag cgatagcgga gtgtatactg   3660

gcttaactat gcggcatcag agcagattgt actgagagtg caccatatat gcggtgtgaa   3720

ataccgcaca gatgcgtaag gagaaaatac cgcatcaggc gctcttccgc ttcctcgctc   3780

actgactcgc tgcgctcggt cgttcggctg cggcgagcgg tatcagctca ctcaaaggcg   3840

gtaatacggt tatccacaga atcaggggat aacgcaggaa agaacatgtg agcaaaaggc   3900

cagcaaaagg ccaggaaccg taaaaaggcc gcgttgctgg cgtttttcca taggctccgc   3960

ccccctgacg agcatcacaa aaatcgacgc tcaagtcaga ggtggcgaaa cccgacagga   4020

ctataaagat accaggcgtt ccccctgga agctccctcg tgcgctctcc tgttccgacc   4080

ctgccgctta ccggatacct gtccgccttt ctcccttcgg gaagcgtggc gctttctcat   4140

agctcacgct gtaggtatct cagttcggtg taggtcgttc gctccaagct gggctgtgtg   4200

cacgaacccc ccgttcagcc cgaccgctgc gccttatccg gtaactatcg tcttgagtcc   4260

aacccggtaa gacacgactt atcgccactg gcagcagcca ctggtaacag gattagcaga   4320

gcgaggtatg taggcggtgc tacagagttc ttgaagtggt ggcctaacta cggctacact   4380

agaaggacag tatttggtat ctgcgctctg ctgaagccag ttaccttcgg aaaaagagtt   4440

ggtagctctt gatccggcaa acaaaccacc gctggtagcg gtggtttttt tgtttgcaag   4500

cagcagatta cgcgcagaaa aaaaggatct caagaagatc ctttgatctt ttctacgggg   4560

tctgacgctc agtggaacga aaactcacgt taagggattt tggtcatgaa caataaaact   4620

gtctgcttac ataaacagta atacaagggg tgttatgagc catattcaac gggaaacgtc   4680

ttgctctagg ccgcgattaa attccaacat ggatgctgat ttatatgggt ataaatgggc   4740

tcgcgataat gtcgggcaat caggtgcgac aatctatcga ttgtatggga gcccgatgc   4800

gccagagttg tttctgaaac atggcaaagg tagcgttgcc aatgatgtta cagatgagat   4860

ggtcagacta aactggctga cggaatttat gcctcttccg accatcaagc attttatccg   4920

tactcctgat gatgcatggt tactcaccac tgcgatcccc gggaaaacag cattccaggt   4980

attagaagaa tatcctgatt caggtgaaaa tattgttgat gcgctggcag tgttcctgcg   5040

ccggttgcat tcgattcctg tttgtaattg tccttttaac agcgatcgcg tatttcgtct   5100

cgctcaggcg caatcacgaa tgaataacgg tttggttgat gcgagtgatt ttgatgacga   5160

gcgtaatggc tggcctgttg aacaagtctg gaaagaaatg cataaacttt tgccattctc   5220

accggattca gtcgtcactc atggtgattt ctcacttgat aaccttattt ttgacgaggg   5280
```

```
gaaattaata ggttgtattg atgttggacg agtcggaatc gcagaccgat accaggatct    5340

tgccatccta tggaactgcc tcggtgagtt ttctccttca ttacagaaac ggctttttca    5400

aaaatatggt attgataatc ctgatatgaa taaattgcag tttcatttga tgctcgatga    5460

gttttttctaa gaattaattc atgagcggat acatatttga atgtatttag aaaaataaac    5520

aaataggggt tccgcgcaca tttccccgaa aagtgccacc tgaaattgta aacgttaata    5580

ttttgttaaa attcgcgtta aattttttgtt aaatcagctc attttttaac caataggccg    5640

aaatcggcaa aatcccttat aaatcaaaag aatagaccga gatagggttg agtgttgttc    5700

cagtttggaa caagagtcca ctattaaaga acgtggactc caacgtcaaa gggcgaaaaa    5760

ccgtctatca gggcgatggc ccactacgtg aaccatcacc ctaatcaagt ttttttgggggt   5820

cgaggtgccg taaagcacta aatcggaacc ctaaagggag cccccgattt agagcttgac    5880

ggggaaagcc ggcgaacgtg gcgagaaagg aagggaagaa agcgaaagga gcgggcgcta    5940

gggcgctggc aagtgtagcg gtcacgctgc gcgtaaccac cacacccgcc gcgcttaatg    6000

cgccgctaca gggcgcgtcc cattcgcca                                      6029
```

```
<210>  3
<211>  5369
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Intermediate pETM-adp plasmid, on way to pETM-GFP-Imm construct

<400>  3
catcaccatc accatcaccc catgagcgat tacgacatcc ccactactga gaatctttat     60

tttcagggcg ccatgggagg cacggtaccg gatccgaatt cgagctccgt cgacaagctt    120

gcggccgcac tcgagcacca ccaccaccac cactgagatc cggctgctaa caaagcccga    180

aaggaagctg agttggctgc tgccaccgct gagcaataac tagcataacc ccttggggcc    240

tctaaacggg tcttgagggg tttttttgctg aaaggaggaa ctatatccgg attggcgaat    300

gggacgcgcc ctgtagcggc gcattaagcg cggcgggtgt ggtggttacg cgcagcgtga    360

ccgctacact tgccagcgcc ctagcgcccg ctcctttcgc tttcttccct tcctttctcg    420

ccacgttcgc cggctttccc cgtcaagctc taaatcgggg gctccctttta gggttccgat    480

ttagtgcttt acggcacctc gacccccaaaa aacttgatta gggtgatggt tcacgtagtg    540

ggccatcgcc ctgatagacg gtttttcgcc ctttgacgtt ggagtccacg ttctttaata    600

gtggactctt gttccaaact ggaacaacac tcaaccctat ctcggtctat tcttttgatt    660

tataagggat tttgccgatt tcggcctatt ggttaaaaaa tgagctgatt taacaaaaat    720

ttaacgcgaa ttttaacaaa atattaacgt ttacaatttc aggtggcact tttcggggaa    780

atgtgcgcgg aacccctatt tgtttatttt tctaaataca ttcaaatatg tatccgctca    840
```

```
tgaattaatt cttagaaaaa ctcatcgagc atcaaatgaa actgcaattt attcatatca    900

ggattatcaa taccatattt ttgaaaaagc cgtttctgta atgaaggaga aaactcaccg    960

aggcagttcc ataggatggc aagatcctgg tatcggtctg cgattccgac tcgtccaaca   1020

tcaatacaac ctattaattt cccctcgtca aaaataaggt tatcaagtga gaaatcacca   1080

tgagtgacga ctgaatccgg tgagaatggc aaaagtttat gcatttcttt ccagacttgt   1140

tcaacaggcc agccattacg ctcgtcatca aaatcactcg catcaaccaa accgttattc   1200

attcgtgatt gcgcctgagc gagacgaaat acgcgatcgc tgttaaaagg acaattacaa   1260

acaggaatcg aatgcaaccg gcgcaggaac actgccagcg catcaacaat attttcacct   1320

gaatcaggat attcttctaa tacctggaat gctgttttcc cggggatcgc agtggtgagt   1380

aaccatgcat catcaggagt acggataaaa tgcttgatgg tcggaagagg cataaattcc   1440

gtcagccagt ttagtctgac catctcatct gtaacatcat tggcaacgct acctttgcca   1500

tgtttcagaa acaactctgg cgcatcgggc ttcccataca atcgatagat tgtcgcacct   1560

gattgcccga cattatcgcg agcccattta tacccatata aatcagcatc catgttggaa   1620

tttaatcgcg gcctagagca agacgtttcc cgttgaatat ggctcataac accccttgta   1680

ttactgtttta tgtaagcaga cagttttatt gttcatgacc aaaatccctt aacgtgagtt   1740

ttcgttccac tgagcgtcag accccgtaga aaagatcaaa ggatcttctt gagatccttt   1800

ttttctgcgc gtaatctgct gcttgcaaac aaaaaaacca ccgctaccag cggtggtttg   1860

tttgccggat caagagctac caactctttt tccgaaggta actggcttca gcagagcgca   1920

gataccaaat actgtccttc tagtgtagcc gtagttaggc caccacttca agaactctgt   1980

agcaccgcct acatacctcg ctctgctaat cctgttacca gtggctgctg ccagtggcga   2040

taagtcgtgt cttaccgggt tggactcaag acgatagtta ccggataagg cgcagcggtc   2100

gggctgaacg ggggggttcgt gcacacagcc cagcttggag cgaacgacct acaccgaact   2160

gagataccta cagcgtgagc tatgagaaag cgccacgctt cccgaaggga aaaggcgga    2220

caggtatccg gtaagcggca gggtcggaac aggagagcgc acgagggagc ttccaggggg   2280

aaacgcctgg tatctttata gtcctgtcgg gtttcgccac ctctgacttg agcgtcgatt   2340

tttgtgatgc tcgtcagggg ggcggagcct atggaaaaac gccagcaacg cggcctttt    2400

acggttcctg ccttttgct ggccttttgc tcacatgttc tttcctgcgt tatcccctga    2460

ttctgtggat aaccgtatta ccgcctttga gtgagctgat accgctcgcc gcagccgaac   2520

gaccgagcgc agcgagtcag tgagcgagga agcggaagag cgcctgatgc ggtattttct   2580

ccttacgcat ctgtgcggta tttcacaccg catatatggt gcactctcag tacaatctgc   2640

tctgatgccg catagttaag ccagtataca ctccgctatc gctacgtgac tgggtcatgg   2700
```

Page 6

```
ctgcgccccg acacccgcca acacccgctg acgcgccctg acgggcttgt ctgctcccgg    2760

catccgctta cagacaagct gtgaccgtct ccgggagctg catgtgtcag aggttttcac    2820

cgtcatcacc gaaacgcgcg aggcagctgc ggtaaagctc atcagcgtgg tcgtgaagcg    2880

attcacagat gtctgcctgt tcatccgcgt ccagctcgtt gagtttctcc agaagcgtta    2940

atgtctggct tctgataaag cgggccatgt taagggcggt tttttcctgt ttggtcactg    3000

atgcctccgt gtaaggggga tttctgttca tgggggtaat gataccgatg aaacgagaga    3060

ggatgctcac gatacgggtt actgatgatg aacatgcccg gttactggaa cgttgtgagg    3120

gtaaacaact ggcggtatgg atgcggcggg accagagaaa aatcactcag ggtcaatgcc    3180

agcgcttcgt taatacagat gtaggtgttc cacagggtag ccagcagcat cctgcgatgc    3240

agatccggaa cataatggtg cagggcgctg acttccgcgt ttccagactt tacgaaacac    3300

ggaaaccgaa gaccattcat gttgttgctc aggtcgcaga cgttttgcag cagcagtcgc    3360

ttcacgttcg ctcgcgtatc ggtgattcat tctgctaacc agtaaggcaa ccccgccagc    3420

ctagccgggt cctcaacgac aggagcacga tcatgcgcac ccgtggggcc gccatgccgg    3480

cgataatggc ctgcttctcg ccgaaacgtt tggtggcggg accagtgacg aaggcttgag    3540

cgagggcgtg caagattccg aataccgcaa gcgacaggcc gatcatcgtc gcgctccagc    3600

gaaagcggtc ctcgccgaaa atgacccaga gcgctgccgg cacctgtcct acgagttgca    3660

tgataaagaa gacagtcata agtgcggcga cgatagtcat gccccgcgcc caccggaagg    3720

agctgactgg gttgaaggct ctcaagggca tcggtcgaga tcccggtgcc taatgagtga    3780

gctaacttac attaattgcg ttgcgctcac tgcccgcttt ccagtcggga aacctgtcgt    3840

gccagctgca ttaatgaatc ggccaacgcg cggggagagg cggtttgcgt attgggcgcc    3900

agggtggttt ttcttttcac cagtgagacg ggcaacagct gattgccctt caccgcctgg    3960

ccctgagaga gttgcagcaa gcggtccacg ctggtttgcc ccagcaggcg aaaatcctgt    4020

ttgatggtgg ttaacggcgg gatataacat gagctgtctt cggtatcgtc gtatcccact    4080

accgagatat ccgcaccaac gcgcagcccg gactcggtaa tggcgcgcat tgcgcccagc    4140

gccatctgat cgttggcaac cagcatcgca gtgggaacga tgccctcatt cagcatttgc    4200

atggtttgtt gaaaaccgga catggcactc cagtcgcctt cccgttccgc tatcggctga    4260

atttgattgc gagtgagata tttatgccag ccagccagac gcagacgcgc cgagacagaa    4320

cttaatgggc ccgctaacag cgcgatttgc tggtgaccca atgcgaccag atgctccacg    4380

cccagtcgcg taccgtcttc atgggagaaa ataatactgt tgatgggtgt ctggtcagag    4440

acatcaagaa ataacgccgg aacattagtg caggcagctt ccacagcaat ggcatcctgg    4500

tcatccagcg gatagttaat gatcagccca ctgacgcgtt gcgcgagaag attgtgcacc    4560

gccgctttac aggcttcgac gccgcttcgt tctaccatcg acaccaccac gctggcaccc    4620
```

Page 7

```
agttgatcgg cgcgagattt aatcgccgcg acaatttgcg acggcgcgtg cagggccaga     4680

ctggaggtgg caacgccaat cagcaacgac tgtttgcccg ccagttgttg tgccacgcgg     4740

ttgggaatgt aattcagctc cgccatcgcc gcttccactt tttcccgcgt tttcgcagaa     4800

acgtggctgg cctggttcac cacgcgggaa acggtctgat aagagacacc ggcatactct     4860

gcgacatcgt ataacgttac tggtttcaca ttcaccaccc tgaattgact ctcttccggg     4920

cgctatcatg ccataccgcg aaaggttttg cgccattcga tggtgtccgg gatctcgacg     4980

ctctccctta tgcgactcct gcattaggaa gcagcccagt agtaggttga ggccgttgag     5040

caccgccgcc gcaaggaatg gtgcatgcaa ggagatggcg cccaacagtc ccccggccac     5100

ggggcctgcc accataccca cgccgaaaca agcgctcatg agcccgaagt ggcgagcccg     5160

atcttcccca tcggtgatgt cggcgatata ggcgccagca accgcacctg tggcgccggt     5220

gatgccggcc acgatgcgtc cggcgtagag gatcgagatc tcgatcccgc gaaattaata     5280

cgactcacta tagggggaatt gtgagcggat aacaattccc ctctagaaat aattttgatt     5340

taactttaag aaggagatat accatgaaa                                        5369
```

```
<210>  4
<211>  3337
<212>  DNA
<213>  Artificial sequence

<220>
<223>  pGFPuv plasmid coding for GFP from Aequorea victoria


<220>
<221>  CDS
<222>  (286)..(1014)
<223>  pGFPuv plasmid coding for GFP from Aequorea victoria

<400>  4
agcgcccaat acgcaaaccg cctctccccg cgcgttggcc gattcattaa tgcagctggc     60

acgacaggtt tcccgactgg aaagcgggca gtgagcgcaa cgcaattaat gtgagttagc     120

tcactcatta ggcaccccag gctttacact ttatgcttcc ggctcgtatg ttgtgtggaa     180

ttgtgagcgg ataacaattt cacacaggaa acagctatga ccatgattac gccaagcttg     240

catgcctgca ggtcgactct agaggatccc cgggtaccgg tagaa aaa atg agt aaa     297
                                                       Lys Met Ser Lys
                                                         1

gga gaa gaa ctt ttc act gga gtt gtc cca att ctt gtt gaa tta gat       345
Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
 5               10              15              20

ggt gat gtt aat ggg cac aaa ttt tct gtc agt gga gag ggt gaa ggt       393
Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
            25              30              35
```

Page 8

```
gat gca aca tac gga aaa ctt acc ctt aaa ttt att tgc act act gga    441
Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
        40              45              50

aaa cta cct gtt cca tgg cca aca ctt gtc act act ttc tct tat ggt    489
Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly
        55              60              65

gtt caa tgc ttt tcc cgt tat ccg gat cat atg aaa cgg cat gac ttt    537
Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe
        70              75              80

ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa cgc act ata tct    585
Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Ser
85              90              95              100

ttc aaa gat gac ggg aac tac aag acg cgt gct gaa gtc aag ttt gaa    633
Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
            105             110             115

ggt gat acc ctt gtt aat cgt atc gag tta aaa ggt att gat ttt aaa    681
Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
            120             125             130

gaa gat gga aac att ctc gga cac aaa ctc gag tac aac tat aac tca    729
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
            135             140             145

cac aat gta tac atc acg gca gac aaa caa aag aat gga atc aaa gct    777
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
    150             155             160

aac ttc aaa att cgc cac aac att gaa gat gga tcc gtt caa cta gca    825
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
165             170             175             180

gac cat tat caa caa aat act cca att ggc gat ggc cct gtc ctt tta    873
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
                185             190             195

cca gac aac cat tac ctg tcg aca caa tct gcc ctt tcg aaa gat ccc    921
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
            200             205             210

aac gaa aag cgt gac cac atg gtc ctt ctt gag ttt gta act gct gct    969
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
        215             220             225

ggg att aca cat ggc atg gat gag ctc tac aaa taa tga att cca        1014
Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys         Ile Pro
        230             235             240

actgagcgcc ggtcgctacc attaccaact tgtctggtgt caaaaataat aggcctacta   1074

gtcggccgta cgggcccttt cgtctcgcgc gtttcggtga tgacggtgaa aacctctgac   1134

acatgcagct cccggagacg gtcacagctt gtctgtaagc ggatgccggg agcagacaag   1194

cccgtcaggg cgcgtcagcg ggtgttggcg ggtgtcgggg ctggcttaac tatgcggcat   1254

cagagcagat tgtactgaga gtgcaccata tgcggtgtga ataccgcac agatgcgtaa   1314

ggagaaaata ccgcatcagg cggccttaag ggcctcgtga tacgcctatt tttataggtt   1374
```
Page 9

```
aatgtcatga taataatggt ttcttagacg tcaggtggca ctttcggggg aaatgtgcgc    1434

ggaacccta tttgtttatt tttctaaata cattcaaata tgtatccgct catgagacaa     1494

taaccctgat aaatgcttca ataatattga aaaaggaaga gtatgagtat tcaacatttc    1554

cgtgtcgccc ttattcctt ttttgcggca ttttgccttc ctgtttttgc tcacccagaa     1614

acgctggtga aagtaaaaga tgctgaagat cagttgggtg cacgagtggg ttacatcgaa    1674

ctggatctca acagcggtaa gatccttgag agttttcgcc ccgaagaacg ttttccaatg    1734

atgagcactt ttaaagttct gctatgtggc gcggtattat cccgtattga cgccgggcaa    1794

gagcaactcg gtcgccgcat acactattct cagaatgact tggttgagta ctcaccagtc    1854

acagaaaagc atcttacgga tggcatgaca gtaagagaat tatgcagtgc tgccataacc    1914

atgagtgata acactgcggc caacttactt ctgacaacga tcggaggacc gaaggagcta    1974

accgcttttt tgcacaacat ggggggatcat gtaactcgcc ttgatcgttg ggaaccggag    2034

ctgaatgaag ccataccaaa cgacgagcgt gacaccacga tgcctgtagc aatggcaaca    2094

acgttgcgca aactattaac tggcgaacta cttactctag cttcccggca acaattaata    2154

gactggatgg aggcggataa agttgcagga ccacttctgc gctcggccct tccggctggc    2214

tggtttattg ctgataaatc tggagccggt gagcgtgggt ctcgcggtat cattgcagca    2274

ctggggccag atggtaagcc ctcccgtatc gtagttatct acacgacggg gagtcaggca    2334

actatggatg aacgaaatag acagatcgct gagataggtg cctcactgat taagcattgg    2394

taactgtcag accaagttta ctcatatata ctttagattg atttaaaact tcatttttaa    2454

tttaaaagga tctaggtgaa gatcctttt gataatctca tgaccaaaat cccttaacgt     2514

gagttttcgt tccactgagc gtcagacccc gtagaaaaga tcaaaggatc ttcttgagat    2574

ccttttttc tgcgcgtaat ctgctgcttg caaacaaaaa aaccaccgct accagcggtg     2634

gtttgtttgc cggatcaaga ctaccaact ctttttccga aggtaactgg cttcagcaga     2694

gcgcagatac caaatactgt ccttctagtg tagccgtagt taggccacca cttcaagaac    2754

tctgtagcac cgcctacata cctcgctctg ctaatcctgt taccagtggc tgctgccagt    2814

ggcgataagt cgtgtcttac cgggttggac tcaagacgat agttaccgga taaggcgcag    2874

cggtcgggct gaacgggggg ttcgtgcaca cagcccagct tggagcgaac gacctacacc    2934

gaactgagat acctacagcg tgagctatga gaaagcgcca cgcttcccga agggagaaag    2994

gcggacaggt atccggtaag cggcagggtc ggaacaggag agcgcacgag ggagcttcca    3054

gggggaaacg cctggtatct ttatagtcct gtcgggtttc gccacctctg acttgagcgt    3114

cgattttgt gatgctcgtc agggggcgg agcctatgga aaaacgccag caacgcggcc      3174

ttttacggt tcctggcctt ttgctggcct tttgctcaca tgttctttcc tgcgttatcc     3234
```

cctgattctg tggataaccg tattaccgcc tttgagtgag ctgataccgc tcgccgcagc   3294

cgaacgaccg agcgcagcga gtcagtgagc gaggaagcgg aag   3337

<210> 5
<211> 239
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 5

Lys Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1   5   10   15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                20   25   30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
            35   40   45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
        50   55   60

Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65   70   75   80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85   90   95

Arg Thr Ile Ser Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
                100   105   110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
            115   120   125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
        130   135   140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145   150   155   160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165   170   175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
            180   185   190

```
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
        195                 200                 205


Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
    210                 215                 220


Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225                 230                 235
```

```
<210>  6
<211>  6069
<212>  DNA
<213>  Artificial sequence

<220>
<223>  pETM-GFP-Imm plasmid containing Hisx6 tag, flexible joint

       as frame adapter, and A. victoria GFP gene


<220>
<221>  CDS
<222>  (1)..(876)
<223>  pETM-GFP-Imm plasmid containing Hisx6 tag, flexible joint

       as frame adapter, and A. victoria GFP gene

<400>  6
atg aaa cat cac cat cac cat cac ccc atg agc gat tac gac atc ccc      48
Met Lys His His His His His His Pro Met Ser Asp Tyr Asp Ile Pro
1               5                   10                  15

act act gag aat ctt tat ttt cag ggc gcc atg gga ggc acg gta ccg      96
Thr Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Gly Gly Thr Val Pro
            20                  25                  30

gta gaa aaa atg agt aaa gga gaa gaa ctt ttc act gga gtt gtc cca     144
Val Glu Lys Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
        35                  40                  45

att ctt gtt gaa tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc     192
Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
    50                  55                  60

agt gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa     240
Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
65                  70                  75                  80

ttt att tgc act act gga aaa cta cct gtt cca tgg cca aca ctt gtc     288
Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
                85                  90                  95

act act ttc tct tat ggt gtt caa tgc ttt tcc cgt tat ccg gat cat     336
Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
            100                 105                 110

atg aaa cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta     384
Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
            115                 120                 125
```

```
cag gaa cgc act ata tct ttc aaa gat gac ggg aac tac aag acg cgt        432
Gln Glu Arg Thr Ile Ser Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
    130                 135                 140

gct gaa gtc aag ttt gaa ggt gat acc ctt gtt aat cgt atc gag tta        480
Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
145                 150                 155                 160

aaa ggt att gat ttt aaa gaa gat gga aac att ctc gga cac aaa ctc        528
Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
                    165                 170                 175

gag tac aac tat aac tca cac aat gta tac atc acg gca gac aaa caa        576
Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
                180                 185                 190

aag aat gga atc aaa gct aac ttc aaa att cgc cac aac att gaa gat        624
Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
            195                 200                 205

gga tcc gtt caa cta gca gac cat tat caa caa aat act cca att ggc        672
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
        210                 215                 220

gat ggc cct gtc ctt tta cca gac aac cat tac ctg tcg aca caa tct        720
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
225                 230                 235                 240

gcc ctt tcg aaa gat ccc aac gaa aag cgt gac cac atg gtc ctt ctt        768
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
                    245                 250                 255

gag ttt gta act gct gct ggg att aca cat ggc atg gat gag ctc cgt        816
Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Arg
                260                 265                 270

cga caa gct tgc ggc cgc act cga gca cca cca cca cca cca ctg aga        864
Arg Gln Ala Cys Gly Arg Thr Arg Ala Pro Pro Pro Pro Pro Leu Arg
            275                 280                 285

tcc ggc tgc taa caaagcccga aggaagctg agttggctgc tgccaccgct          916
Ser Gly Cys
    290

gagcaataac tagcataacc ccttggggcc tctaaacggg tcttgagggg ttttttgctg      976

aaaggaggaa ctatatccgg attggcgaat gggacgcgcc ctgtagcggc gcattaagcg     1036

cggcgggtgt ggtggttacg cgcagcgtga ccgctacact tgccagcgcc ctagcgcccg     1096

ctcctttcgc tttcttccct tcctttctcg ccacgttcgc cggctttccc cgtcaagctc     1156

taaatcgggg gctcccttta gggttccgat ttagtgcttt acggcacctc gaccccaaaa     1216

aacttgatta gggtgatggt tcacgtagtg ggccatcgcc ctgatagacg gtttttcgcc     1276

ctttgacgtt ggagtccacg ttctttaata gtggactctt gttccaaact ggaacaacac     1336

tcaaccctat ctcggtctat tcttttgatt tataagggat tttgccgatt tcggcctatt     1396

ggttaaaaaa tgagctgatt taacaaaaat ttaacgcgaa ttttaacaaa atattaacgt     1456

ttacaatttc aggtggcact tttcggggaa atgtgcgcgg aacccctatt tgtttatttt     1516
```
                                    Page 13

tctaaataca ttcaaatatg tatccgctca tgaattaatt cttagaaaaa ctcatcgagc 1576

atcaaatgaa actgcaattt attcatatca ggattatcaa taccatattt ttgaaaaagc 1636

cgtttctgta atgaaggaga aaactcaccg aggcagttcc ataggatggc aagatcctgg 1696

tatcggtctg cgattccgac tcgtccaaca tcaatacaac ctattaattt cccctcgtca 1756

aaaataaggt tatcaagtga gaaatcacca tgagtgacga ctgaatccgg tgagaatggc 1816

aaaagtttat gcatttcttt ccagacttgt tcaacaggcc agccattacg ctcgtcatca 1876

aaatcactcg catcaaccaa accgttattc attcgtgatt gcgcctgagc gagacgaaat 1936

acgcgatcgc tgttaaaagg acaattacaa acaggaatcg aatgcaaccg gcgcaggaac 1996

actgccagcg catcaacaat attttcacct gaatcaggat attcttctaa tacctggaat 2056

gctgtttttcc cggggatcgc agtggtgagt aaccatgcat catcaggagt acggataaaa 2116

tgcttgatgg tcggaagagg cataaattcc gtcagccagt ttagtctgac catctcatct 2176

gtaacatcat tggcaacgct acctttgcca tgtttcagaa acaactctgg cgcatcgggc 2236

ttcccataca atcgatagat tgtcgcacct gattgcccga cattatcgcg agcccattta 2296

tacccatata aatcagcatc catgttggaa tttaatcgcg gcctagagca agacgtttcc 2356

cgttgaatat ggctcataac accccttgta ttactgttta tgtaagcaga cagttttatt 2416

gttcatgacc aaaatccctt aacgtgagtt ttcgttccac tgagcgtcag accccgtaga 2476

aaagatcaaa ggatcttctt gagatccttt ttttctgcgc gtaatctgct gcttgcaaac 2536

aaaaaaacca ccgctaccag cggtggtttg tttgccggat caagagctac caactctttt 2596

tccgaaggta actggcttca gcagagcgca gataccaaat actgtccttc tagtgtagcc 2656

gtagttaggc caccacttca agaactctgt agcaccgcct acatacctcg ctctgctaat 2716

cctgttacca gtggctgctg ccagtggcga taagtcgtgt cttaccgggt tggactcaag 2776

acgatagtta ccggataagg cgcagcggtc gggctgaacg gggggttcgt gcacacagcc 2836

cagcttggag cgaacgacct acaccgaact gagataccta cagcgtgagc tatgagaaag 2896

cgccacgctt cccgaaggga gaaaggcgga caggtatccg gtaagcggca gggtcggaac 2956

aggagagcgc acgagggagc ttccaggggg aaacgcctgg tatctttata gtcctgtcgg 3016

gtttcgccac ctctgacttg agcgtcgatt tttgtgatgc tcgtcagggg ggcggagcct 3076

atggaaaaac gccagcaacg cggccttttt acggttcctg ccttttgct ggccttttgc 3136

tcacatgttc tttcctgcgt tatcccctga ttctgtggat aaccgtatta ccgcctttga 3196

gtgagctgat accgctcgcc gcagccgaac gaccgagcgc agcgagtcag tgagcgagga 3256

agcggaagag cgcctgatgc ggtattttct ccttacgcat ctgtgcggta tttcacaccg 3316

catatatggt gcactctcag tacaatctgc tctgatgccg catagttaag ccagtataca 3376

```
ctccgctatc gctacgtgac tgggtcatgg ctgcgccccg acacccgcca acacccgctg    3436

acgcgccctg acgggcttgt ctgctcccgg catccgctta cagacaagct gtgaccgtct    3496

ccgggagctg catgtgtcag aggttttcac cgtcatcacc gaaacgcgcg aggcagctgc    3556

ggtaaagctc atcagcgtgg tcgtgaagcg attcacagat gtctgcctgt tcatccgcgt    3616

ccagctcgtt gagtttctcc agaagcgtta atgtctggct tctgataaag cgggccatgt    3676

taagggcggt tttttcctgt ttggtcactg atgcctccgt gtaaggggga tttctgttca    3736

tgggggtaat gataccgatg aaacgagaga ggatgctcac gatacgggtt actgatgatg    3796

aacatgcccg gttactggaa cgttgtgagg gtaaacaact ggcggtatgg atgcggcggg    3856

accagagaaa aatcactcag ggtcaatgcc agcgcttcgt taatacagat gtaggtgttc    3916

cacagggtag ccagcagcat cctgcgatgc agatccggaa cataatggtg cagggcgctg    3976

acttccgcgt ttccagactt tacgaaacac ggaaaccgaa gaccattcat gttgttgctc    4036

aggtcgcaga cgttttgcag cagcagtcgc ttcacgttcg ctcgcgtatc ggtgattcat    4096

tctgctaacc agtaaggcaa ccccgccagc ctagccgggt cctcaacgac aggagcacga    4156

tcatgcgcac ccgtggggcc gccatgccgg cgataatggc ctgcttctcg ccgaaacgtt    4216

tggtggcggg accagtgacg aaggcttgag cgagggcgtg caagattccg aataccgcaa    4276

gcgacaggcc gatcatcgtc gcgctccagc gaaagcggtc ctcgccgaaa atgacccaga    4336

gcgctgccgg cacctgtcct acgagttgca tgataaagaa gacagtcata agtgcggcga    4396

cgatagtcat gccccgcgcc caccggaagg agctgactgg gttgaaggct ctcaagggca    4456

tcggtcgaga tcccggtgcc taatgagtga gctaacttac attaattgcg ttgcgctcac    4516

tgcccgcttt ccagtcggga aacctgtcgt gccagctgca ttaatgaatc ggccaacgcg    4576

cggggagagg cggtttgcgt attgggcgcc agggtggttt ttcttttcac cagtgagacg    4636

ggcaacagct gattgccctt caccgcctgg ccctgagaga gttgcagcaa gcggtccacg    4696

ctggtttgcc ccagcaggcg aaaatcctgt ttgatggtgg ttaacggcgg gatataacat    4756

gagctgtctt cggtatcgtc gtatcccact accgagatat ccgcaccaac gcgcagcccg    4816

gactcggtaa tggcgcgcat tgcgcccagc gccatctgat cgttggcaac cagcatcgca    4876

gtgggaacga tgccctcatt cagcatttgc atggtttgtt gaaaaccgga catggcactc    4936

cagtcgcctt cccgttccgc tatcggctga atttgattgc gagtgagata tttatgccag    4996

ccagccagac gcagacgcgc cgagacagaa cttaatgggc ccgctaacag cgcgatttgc    5056

tggtgaccca atgcgaccag atgctccacg cccagtcgcg taccgtcttc atgggagaaa    5116

ataatactgt tgatgggtgt ctggtcagag acatcaagaa ataacgccgg aacattagtg    5176

caggcagctt ccacagcaat ggcatcctgg tcatccagcg gatagttaat gatcagccca    5236

ctgacgcgtt gcgcgagaag attgtgcacc gccgctttac aggcttcgac gccgcttcgt    5296
```

```
tctaccatcg acaccaccac gctggcaccc agttgatcgg cgcgagattt aatcgccgcg    5356

acaatttgcg acggcgcgtg cagggccaga ctggaggtgg caacgccaat cagcaacgac    5416

tgtttgcccg ccagttgttg tgccacgcgg ttgggaatgt aattcagctc cgccatcgcc    5476

gcttccactt tttcccgcgt tttcgcagaa acgtggctgg cctggttcac cacgcgggaa    5536

acggtctgat aagagacacc ggcatactct gcgacatcgt ataacgttac tggtttcaca    5596

ttcaccaccc tgaattgact ctcttccggg cgctatcatg ccataccgcg aaaggttttg    5656

cgccattcga tggtgtccgg gatctcgacg ctctccctta tgcgactcct gcattaggaa    5716

gcagcccagt agtaggttga ggccgttgag caccgccgcc gcaaggaatg gtgcatgcaa    5776

ggagatggcg cccaacagtc ccccggccac ggggcctgcc accataccca cgccgaaaca    5836

agcgctcatg agcccgaagt ggcgagcccg atcttcccca tcggtgatgt cggcgatata    5896

ggcgccagca accgcacctg tggcgccggt gatgccggcc acgatgcgtc cggcgtagag    5956

gatcgagatc tcgatcccgc gaaattaata cgactcacta tagggaatt gtgagcggat    6016

aacaattccc ctctagaaat aattttgatt taactttaag aaggagatat acc           6069
```

<210> 7
<211> 291
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 7

```
Met Lys His His His His His His Pro Met Ser Asp Tyr Asp Ile Pro
1               5                   10                  15


Thr Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Gly Gly Thr Val Pro
            20                  25                  30


Val Glu Lys Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
        35                  40                  45


Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
    50                  55                  60


Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
65                  70                  75                  80


Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
                85                  90                  95


Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
```

Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
        115   120   125

Gln Glu Arg Thr Ile Ser Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
    130   135   140

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
145   150   155   160

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
            165   170   175

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
            180   185   190

Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
        195   200   205

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
    210   215   220

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
225   230   235   240

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
            245   250   255

Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Arg
            260   265   270

Arg Gln Ala Cys Gly Arg Thr Arg Ala Pro Pro Pro Pro Pro Leu Arg
        275   280   285

Ser Gly Cys
    290

<210> 8
<211> 17
<212> DNA
<213> Artificial sequence

<220>
<223> Frame adapter used for prevention of frameshift mutation as a
       result of plasmid modification

<220>

```
<221>  misc_feature
<222>  (1)..(17)
<223>  Frame adapter used for prevention of frameshift mutation as a
       result of plasmid modification

<400>  8                                                            17
catgggaggc acggtac


<210>  9
<211>  5
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Peptide design based on size and flexibility to act as a linker
       between the tag and GFP protein segments


<220>
<221>  MISC_FEATURE
<223>  Peptide design based on size and flexibility to act as a linker
       between the tag and GFP protein segments

<400>  9

Met Gly Gly Thr Val
1               5


<210>  10
<211>  6
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Peptide design based on charge and shape to bind the

       expressed protein to a suitably interactive surface


<220>
<221>  MISC_FEATURE
<223>  Peptide design based on charge and shape to bind the

       expressed protein to a suitably interactive surface

<400>  10

His His His His His His
1               5


<210>  11
<211>  238
<212>  PRT
<213>  Aequorea victora


<220>
<221>  MISC_FEATURE
<223>  Green fluorescent peptide coded by pGFPuv plasmid, permitting
```

easy visualisation and quantification based on fluorescence
properties

<400> 11

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1   5   10   15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20   25   30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35   40   45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50   55   60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65   70   75   80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85   90   95

Thr Ile Ser Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100   105   110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115   120   125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130   135   140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145   150   155   160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165   170   175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
            180   185   190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
        195   200   205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
    210   215   220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225   230   235

<210> 12
<211> 291
<212> PRT
<213> Artificial sequence

<220>
<223> Completed peptide based on Hisx6 tag, short physically flexible
      linker and green fluorescent protein coded by pETM-GFP-Imm to
      impart fluorescence properties, allowing easy immobilisation with
      retention of bioactivity, visualisation and quantification

<220>
<221> MISC_FEATURE
<223> Completed peptide based on Hisx6 tag, short physically flexible
      linker and green fluorescent protein coded by pETM-GFP-Imm to
      impart fluorescence properties, allowing easy immobilisation with
      retention of bioactivity, visualisation and quantification

<400> 12

Met Lys His His His His His His Pro Met Ser Asp Tyr Asp Ile Pro
1   5   10   15

Thr Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Gly Gly Thr Val Pro
            20   25   30

Val Glu Lys Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
        35   40   45

Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
    50   55   60

Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
65   70   75   80

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
                85   90   95

Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
                100   105   110

Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
            115   120   125

Gln Glu Arg Thr Ile Ser Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
    130   135   140

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
145   150   155   160

```
Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
              165             170             175

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
              180             185             190

Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
              195             200             205

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
    210             215             220

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
225             230             235             240

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
              245             250             255

Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Arg
              260             265             270

Arg Gln Ala Cys Gly Arg Thr Arg Ala Pro Pro Pro Pro Pro Leu Arg
              275             280             285

Ser Gly Cys
    290
```

```
<210>  13
<211>  29
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Frame adapter

<400>  13

gtacgccatg ggaggcacgg taccttgtg                                           29
```